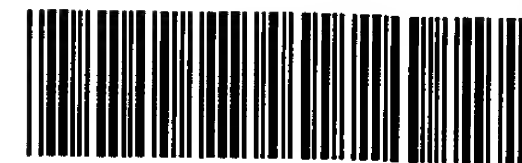


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TECH CENTER 1600/2900

1638



#13 1600

RAW SEQUENCE LISTING

DATE: 08/08/2002

PATENT APPLICATION: US/09/714,767A

TIME: 21:11:09

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\08082002\I714767A.raw

ENTERED

4 <110> APPLICANT: Bidney, Dennis
 5 Duvick, Jon
 6 Hendrick, Carol
 7 Hu, Xu
 8 Lu, Guihua
 9 Crasta, Oswald
 12 <120> TITLE OF INVENTION: Sunflower RhoGAP, LOX, ADH and SCIP -
 13 Polynucleotides and Methods of Use
 16 <130> FILE REFERENCE: 35718/201902
 18 <140> CURRENT APPLICATION NUMBER: 09/714,767A
 19 <141> CURRENT FILING DATE: 2000-11-16
 21 <150> PRIOR APPLICATION NUMBER: US 60/166,128
 22 <151> PRIOR FILING DATE: 1999-11-18
 24 <150> PRIOR APPLICATION NUMBER: US 60/201,837
 25 <151> PRIOR FILING DATE: 2000-05-03
 27 <160> NUMBER OF SEQ ID NOS: 10
 29 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 31 <210> SEQ ID NO: 1
 32 <211> LENGTH: 824
 33 <212> TYPE: DNA
 34 <213> ORGANISM: Helianthus annuus
 36 <220> FEATURE:
 37 <221> NAME/KEY: misc_feature
 38 <222> LOCATION: (0)...(0)
 39 <223> OTHER INFORMATION: rhoGAP
 41 <221> NAME/KEY: CDS
 42 <222> LOCATION: (35)...(637)

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W--> 44 <400> 1

45 ttccggcacga gtccaaatcc aatcttcaat cacc atg gct gaa gaa caa ctg ccg 55
 46 Met Ala Glu Glu Gln Leu Pro
 47 1 5
 49 cct gat caa att aaa ctc att cac aag ctt aat ttg ttc aaa atc aaa 103
 50 Pro Asp Gln Ile Lys Leu Ile His Lys Leu Asn Leu Phe Lys Ile Lys
 51 10 15 20
 53 ggc aga gat aaa cac aat cgc aaa atc tta cga att gtc gga aaa aac 151
 54 Gly Arg Asp Lys His Asn Arg Lys Ile Leu Arg Ile Val Gly Lys Asn
 55 25 30 35
 57 ttt cca gct aag agt ttg acc gtt gac ctg ttg aaa aaa tat cta gaa 199
 58 Phe Pro Ala Lys Ser Leu Thr Val Asp Leu Leu Lys Lys Tyr Leu Glu
 59 40 45 50 55
 61 gtg aaa att ttc ccc aaa ctt gaa cga ccg ttt gtg gtg gtt tac gtt 247
 62 Val Lys Ile Phe Pro Lys Leu Glu Arg Pro Phe Val Val Val Tyr Val
 63 60 65 70

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Input Set : A:\PTO.AMC.txt

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65 cac act gat gtt cag aag agc gag aat ttc cct gga ata tcc gtt ctc      295
66 His Thr Asp Val Gln Lys Ser Glu Asn Phe Pro Gly Ile Ser Val Leu
67          75          80          85
69 cgg tca gtt tac gac gcg att ccg atg acc gtg aaa caa tat ctt gag      343
70 Arg Ser Val Tyr Asp Ala Ile Pro Met Thr Val Lys Gln Tyr Leu Glu
71          90          95          100
73 gcg gtt tac ttt gtt cat ccg gat ctg cag tcc aga att ttt ctg gct      391
74 Ala Val Tyr Phe Val His Pro Asp Leu Gln Ser Arg Ile Phe Leu Ala
75          105          110          115
77 aca ttt ggc cgg ctt atc ttc acc gga ggg tta tat gca aag ctg aga      439
78 Thr Phe Gly Arg Leu Ile Phe Thr Gly Gly Leu Tyr Ala Lys Leu Arg
79 120          125          130          135
81 ttt gtg agt cga ttg gcg tat ctg tgg gaa cat gtg aaa agg aac gag      487
82 Phe Val Ser Arg Leu Ala Tyr Leu Trp Glu His Val Lys Arg Asn Glu
83          140          145          150
85 atc gag atc cca gag ttt gtc tac gat cat gat gag gat ctg gag tac      535
86 Ile Glu Ile Pro Glu Phe Val Tyr Asp His Asp Glu Asp Leu Glu Tyr
87          155          160          165
89 cgt ccg atg atg gat tac ggg ata gag agt gac cac gct aga gtt tat      583
90 Arg Pro Met Met Asp Tyr Gly Ile Glu Ser Asp His Ala Arg Val Tyr
91          170          175          180
93 gga gcg ccc gcg gtt gat tcc tct gtg gcg gct tat tcc atg agg tgt      631
94 Gly Ala Pro Ala Val Asp Ser Ser Val Ala Ala Tyr Ser Met Arg Cys
95          185          190          195
97 atc tca taggggaaat agttgttttt tcttttgttt ttgaaaatag gtgctaaaag      687
98 Ile Ser
99 200
101 aagtgaata tatagtatatt agcaatatatt cgggtgttgt agtatgttga taacgggctt      747
102 ttcttataac attcattggt ctagttttct tttgtaaaaa ttatttgata aattctttgt      807
103 aaaaaaaaaa aaaaaaa      824
105 <210> SEQ ID NO: 2
106 <211> LENGTH: 201
107 <212> TYPE: PRT
108 <213> ORGANISM: Helianthus annus
110 <400> SEQUENCE: 2
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112 1          5          10          15
113 Leu Asn Leu Phe Lys Ile Lys Gly Arg Asp Lys His Asn Arg Lys Ile
114          20          25          30
115 Leu Arg Ile Val Gly Lys Asn Phe Pro Ala Lys Ser Leu Thr Val Asp
116          35          40          45
117 Leu Leu Lys Lys Tyr Leu Glu Val Lys Ile Phe Pro Lys Leu Glu Arg
118          50          55          60
119 Pro Phe Val Val Val Tyr Val His Thr Asp Val Gln Lys Ser Glu Asn
120 65          70          75          80
121 Phe Pro Gly Ile Ser Val Leu Arg Ser Val Tyr Asp Ala Ile Pro Met
122          85          90          95
123 Thr Val Lys Gln Tyr Leu Glu Ala Val Tyr Phe Val His Pro Asp Leu
124          100          105          110

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125 Gln Ser Arg Ile Phe Leu Ala Thr Phe Gly Arg Leu Ile Phe Thr Gly
 126 115 120 125
 127 Gly Leu Tyr Ala Lys Leu Arg Phe Val Ser Arg Leu Ala Tyr Leu Trp
 128 130 135 140
 129 Glu His Val Lys Arg Asn Glu Ile Glu Ile Pro Glu Phe Val Tyr Asp
 130 145 150 155 160
 131 His Asp Glu Asp Leu Glu Tyr Arg Pro Met Met Asp Tyr Gly Ile Glu
 132 165 170 175
 133 Ser Asp His Ala Arg Val Tyr Gly Ala Pro Ala Val Asp Ser Ser Val
 134 180 185 190
 135 Ala Ala Tyr Ser Met Arg Cys Ile Ser
 136 195 200

137 <210> SEQ ID NO: 3

138 <211> LENGTH: 2945

139 <212> TYPE: DNA

140 <213> ORGANISM: Helianthus annuus

142 <220> FEATURE:

143 <221> NAME/KEY: misc_feature

144 <222> LOCATION: (0)...(0)

145 <223> OTHER INFORMATION: lox cDNA

147 <221> NAME/KEY: CDS

148 <222> LOCATION: (19)...(2721)

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 152 Met Leu Asn Ser Gln Ile Asn His Ser His Pro
 153 1 5 10
 155 ctt aac aac cta cta cca atc cgc aaa gcc ttt gtc cat ggt gac acc 99
 156 Leu Asn Asn Leu Leu Pro Ile Arg Lys Ala Phe Val His Gly Asp Thr
 157 15 20 25
 159 act aac cat tcc tcc tcc aac gcc tac tcc ccc gcc aac ctt cgc caa 147
 160 Thr Asn His Ser Ser Ser Asn Ala Tyr Ser Pro Ala Asn Leu Arg Gln
 161 30 35 40
 163 cac gcg tcc acc aag aaa tcc aat gct acc cgt gca cga tcc acc tca 195
 164 His Ala Ser Thr Lys Lys Ser Asn Ala Thr Arg Ala Arg Ser Thr Ser
 165 45 50 55
 167 act gcg ggt aac att aaa gcc ata tca atc ccc ttt ctt acc aag gag 243
 168 Thr Ala Gly Asn Ile Lys Ala Ile Ser Ile Pro Phe Leu Thr Lys Glu
 169 60 65 70 75
 171 acc acc gtc aag tgt gtc atc acc gtc caa cca acc att agt tcc gcc 291
 172 Thr Thr Val Lys Cys Val Ile Thr Val Gln Pro Thr Ile Ser Ser Ala
 173 80 85 90
 175 att gct ggt gta ggc gtt ggt ggt att gtt gat ggt gtt tct gat ctt 339
 176 Ile Ala Gly Val Gly Val Gly Gly Ile Val Asp Gly Val Ser Asp Leu
 177 95 100 105
 179 cta ggg ttg tca ttt ttg ttg gag ctc gtt tca aat gac ctc gat tca 387
 180 Leu Gly Leu Ser Phe Leu Leu Glu Leu Val Ser Asn Asp Leu Asp Ser
 181 110 115 120
 183 aaa gga aac caa aag aca gtg aag gct tat gca aga tac aac gca ctg 435
 184 Lys Gly Asn Gln Lys Thr Val Lys Ala Tyr Ala Arg Tyr Asn Ala Leu

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Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\08082002\I714767A.raw

185	125	130	135	
187	gat ttg gac att agc gtg tac aca tac aaa tgc gac ttc gac gtc cct	483		
188	Asp Leu Asp Ile Ser Val Tyr Thr Tyr Lys Cys Asp Phe Asp Val Pro			
189	140 145 150 155			
191	gaa gat ttt ggg gag ata gga gct gtg ttg gta gaa aat gag tat agc	531		
192	Glu Asp Phe Gly Glu Ile Gly Ala Val Leu Val Glu Asn Glu Tyr Ser			
193	160 165 170			
195	aag aag atg ttt ttc aag aac att gtt ctt aac aac ggt gtt acc ttc	579		
196	Lys Lys Met Phe Phe Lys Asn Ile Val Leu Asn Asn Gly Val Thr Phe			
197	175 180 185			
199	aca tgc gag tca tgg gtt cac tcc aaa tac gat aac cct gag aaa aga	627		
200	Thr Cys Glu Ser Trp Val His Ser Lys Tyr Asp Asn Pro Glu Lys Arg			
201	190 195 200			
203	ata ttt ttc acc gac aag tcg tat cta ccg ttg gaa acg ccg acg gca	675		
204	Ile Phe Phe Thr Asp Lys Ser Tyr Leu Pro Leu Glu Thr Pro Thr Ala			
205	205 210 215			
207	ctg aag ccg tta cga gag aaa gat atg gaa tcg ctt cga gga aac ggc	723		
208	Leu Lys Pro Leu Arg Glu Lys Asp Met Glu Ser Leu Arg Gly Asn Gly			
209	220 225 230 235			
211	gaa gga gaa cgt aaa tca ttc gag cgg ata tat gat tat gat gtg tac	771		
212	Glu Gly Glu Arg Lys Ser Phe Glu Arg Ile Tyr Asp Tyr Asp Val Tyr			
213	240 245 250			
215	aac gat ctc gga gat ccg gat gga agc tta gat cta gca cgg ccg gtg	819		
216	Asn Asp Leu Gly Asp Pro Asp Gly Ser Leu Asp Leu Ala Arg Pro Val			
217	255 260 265			
219	ctc ggt ggc gag aca cat ccg tac cct agg cgg tgc cgt act ggt cgc	867		
220	Leu Gly Gly Glu Thr His Pro Tyr Pro Arg Arg Cys Arg Thr Gly Arg			
221	270 275 280			
223	aaa atg tcc tct aaa gat ccg tta aca gaa agc aga act acg ctc cct	915		
224	Lys Met Ser Ser Lys Asp Pro Leu Thr Glu Ser Arg Thr Thr Leu Pro			
225	285 290 295			
227	ttt tat gta cct gcg gat gaa gat ttt tca gag ata aag agt gtg aac	963		
228	Phe Tyr Val Pro Ala Asp Glu Asp Phe Ser Glu Ile Lys Ser Val Asn			
229	300 305 310 315			
231	ttt gga gca aaa act tta tac tct gtg ctt cat gga gtt gta cca atg	1011		
232	Phe Gly Ala Lys Thr Leu Tyr Ser Val Leu His Gly Val Val Pro Met			
233	320 325 330			
235	cta gac tca att gta aca gac aaa gac aag ggg ttt cca tta ttc aca	1059		
236	Leu Asp Ser Ile Val Thr Asp Lys Asp Lys Gly Phe Pro Leu Phe Thr			
237	335 340 345			
239	tcc ata gat ttg ctt tat aat gaa ggt gtt aat gtt cct tct cct gac	1107		
240	Ser Ile Asp Leu Leu Tyr Asn Glu Gly Val Asn Val Pro Ser Pro Asp			
241	350 355 360			
243	aat gga att cta agt gct tta cct aga ctt gtc aaa ggg gct act gat	1155		
244	Asn Gly Ile Leu Ser Ala Leu Pro Arg Leu Val Lys Gly Ala Thr Asp			
245	365 370 375			
247	gcc gca aat acc gtt atc aag ttc gag acc ccc gaa acc att gat aga	1203		
248	Ala Ala Asn Thr Val Ile Lys Phe Glu Thr Pro Glu Thr Ile Asp Arg			
249	380 385 390 395			

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251	gac	gca	ttc	tca	tgg	ttc	cgt	gat	gaa	gag	ttc	tgc	cgg	caa	atg	ctt	1251
252	Asp	Ala	Phe	Ser	Trp	Phe	Arg	Asp	Glu	Glu	Phe	Cys	Arg	Gln	Met	Leu	
253				400					405					410			
255	gcc	ggt	att	aat	cct	tgt	cgc	ata	caa	ttg	gtt	acg	gaa	tgg	cca	ttg	1299
256	Ala	Gly	Ile	Asn	Pro	Cys	Arg	Ile	Gln	Leu	Val	Thr	Glu	Trp	Pro	Leu	
257				415					420					425			
259	atg	agt	aaa	ctg	gac	cct	gaa	atc	tat	gga	cca	gct	gag	tca	gca	att	1347
260	Met	Ser	Lys	Leu	Asp	Pro	Glu	Ile	Tyr	Gly	Pro	Ala	Glu	Ser	Ala	Ile	
261				430					435					440			
263	aca	aag	gag	att	gta	gag	gaa	gag	att	aaa	ggt	ttc	atg	act	ctt	gag	1395
264	Thr	Lys	Glu	Ile	Val	Glu	Glu	Glu	Ile	Lys	Gly	Phe	Met	Thr	Leu	Glu	
265				445					450					455			
267	gag	gct	tta	gca	caa	aag	aag	ctg	ttt	atg	ctg	gat	tat	cat	gat	ctg	1443
268	Glu	Ala	Leu	Ala	Gln	Lys	Lys	Leu	Phe	Met	Leu	Asp	Tyr	His	Asp	Leu	
269	460					465					470					475	
271	ctc	ttg	cct	tat	gtt	aac	aaa	acg	gag	gct	gaa	ggg	aga	act	ttg	tat	1491
272	Leu	Leu	Pro	Tyr	Val	Asn	Lys	Thr	Glu	Ala	Glu	Gly	Arg	Thr	Leu	Tyr	
273					480						485					490	
275	ggt	tca	aga	act	tta	atg	ttc	ctt	act	cct	gct	gga	aca	tta	agg	cca	1539
276	Gly	Ser	Arg	Thr	Leu	Met	Phe	Leu	Thr	Pro	Ala	Gly	Thr	Leu	Arg	Pro	
277				495						500				505			
279	cta	gcc	att	gag	ctg	act	cgc	cca	cca	gtt	gat	ggg	aaa	cca	cag	tgg	1587
280	Leu	Ala	Ile	Glu	Leu	Thr	Arg	Pro	Pro	Val	Asp	Gly	Lys	Pro	Gln	Trp	
281				510						515				520			
283	aaa	cat	gtt	tac	aca	ccc	gct	tgg	gat	gct	aca	ggt	gca	tgg	ctt	tgg	1635
284	Lys	His	Val	Tyr	Thr	Pro	Ala	Trp	Asp	Ala	Thr	Gly	Ala	Trp	Leu	Trp	
285				525						530				535			
287	aag	cta	gcc	aag	gct	cat	gtc	ctt	gcc	cat	gat	tct	agc	tat	cac	caa	1683
288	Lys	Leu	Ala	Lys	Ala	His	Val	Leu	Ala	His	Asp	Ser	Ser	Tyr	His	Gln	
289	540					545					550					555	
291	ctt	gtt	agc	cat	tgg	cta	aga	aca	cat	tgt	gct	acc	gaa	cct	tac	att	1731
292	Leu	Val	Ser	His	Trp	Leu	Arg	Thr	His	Cys	Ala	Thr	Glu	Pro	Tyr	Ile	
293					560						565					570	
295	att	gct	acc	aat	cgc	caa	ctc	agt	caa	atg	cat	cca	att	cga	cga	ttt	1779
296	Ile	Ala	Thr	Asn	Arg	Gln	Leu	Ser	Gln	Met	His	Pro	Ile	Arg	Arg	Phe	
297				575							580					585	
299	cta	ctc	cct	cat	ttc	cgt	tac	act	atg	caa	att	aat	tct	cta	gct	aga	1827
300	Leu	Leu	Pro	His	Phe	Arg	Tyr	Thr	Met	Gln	Ile	Asn	Ser	Leu	Ala	Arg	
301				590							595					600	
303	ctt	tta	ctc	gtc	aat	gcc	atg	ggt	atc	ata	gag	tca	aca	ttt	tct	cct	1875
304	Leu	Leu	Leu	Val	Asn	Ala	Met	Gly	Ile	Ile	Glu	Ser	Thr	Phe	Ser	Pro	
305				605							610					615	
307	gga	aga	tat	tgt	atg	caa	att	tcc	tct	gat	gca	tat	gat	cag	caa	tgg	1923
308	Gly	Arg	Tyr	Cys	Met	Gln	Ile	Ser	Ser	Asp	Ala	Tyr	Asp	Gln	Gln	Trp	
309	620					625					630					635	
311	cgt	ttt	gat	cat	gaa	gcg	ctt	ccg	gcc	gac	cta	att	agc	agg	ggt	atg	1971
312	Arg	Phe	Asp	His	Glu	Ala	Leu	Pro	Ala	Asp	Leu	Ile	Ser	Arg	Gly	Met	
313					640						645					650	
315	gcg	gtt	gaa	gat	cca	acc	gca	cca	tat	ggt	gta	aaa	cta	aca	atc	gag	2019

VERIFICATION SUMMARY

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Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\08082002\I714767A.raw

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L:150 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3
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L:528 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
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L:731 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:823 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:10
L:827 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:10
L:831 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:10